

#4

SEQUENCE LISTING

<110> ISHIZAKI, JUN  
SUZUKI, NORIKO  
HANASAKI, KOHJI

<120> A GENE ENCODING NOVEL HUMAN SECRETORY TYPE PHOSPHOLIPASE A2

<130> 220738US0PCT

<140> 10/088,092

<141> 2002-03-21

<150> PCT/JP00/06344

<151> 2000-09-18

<150> JP 11-266616

<151> 1999-09-21

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<170> PatentIn version 3.1

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gctatggccg cctgggagaan ctgggctgtg accccaagct ggaaaagtac ctcttctcta	180
tcactcgaga caacatcttc tgtgctggta aaacggcttg ccagcggcat acctgcgaat	240
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ccactacccc aacaagctgt	320

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24

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aggtggcaga	gcaggctccc	atgccccctg	cctacctccc	ccagg atg	aaa cct ccc	177
				Met	Lys Pro Pro	

att gcc ctg gct tgc ctt tgc ctc ctg gtg ccc ctg gct ggc ggg aac	225
Ile Ala Leu Ala Cys Leu Cys Leu Leu Val Pro Leu Ala Gly Gly Asn	
-15 -10 -5 -1 1	

ctg gtc cag ttt gga gtg atg att gag aga atg acg gga aag cct gcc	273
Leu Val Gln Phe Gly Val Met Ile Glu Arg Met Thr Gly Lys Pro Ala	
5 10 15	

ctg cag tac aat gac tat ggc tgc tat tgc ggt gtc ggt ggc tcc cac	321
Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val Gly Gly Ser His	
20 25 30	

tgg cca gtg gac gag acg gat tgg tgt tgt cat gcc cat gac tgc tgc	369
Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala His Asp Cys Cys	
35 40 45	

tat ggc cgc ctg gag aag ctg ggc tgt gac ccc aag ctg gaa aag tac	417
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ctc	ttc	tct	atc	act	cga	gac	aac	atc	ttc	tgt	gct	ggg	aga	acg	gct	465
Leu	Phe	Ser	Ile	Thr	Arg	Asp	Asn	Ile	Phe	Cys	Ala	Gly	Arg	Thr	Ala	
				70					75					80		
tgc	cag	cgg	cat	acc	tgc	gag	tgt	gac	aag	aga	gct	gct	ctt	tgc	ttt	513
Cys	Gln	Arg	His	Thr	Cys	Glu	Cys	Asp	Lys	Arg	Ala	Ala	Leu	Cys	Phe	
			85					90					95			
cgc	cac	aac	ctg	aac	act	tac	aac	cgc	aag	tat	gcc	cac	tac	ccc	aac	561
Arg	His	Asn	Leu	Asn	Thr	Tyr	Asn	Arg	Lys	Tyr	Ala	His	Tyr	Pro	Asn	
		100					105					110				
aag	ctg	tgt	act	ggg	ccc	acc	cca	ccc	tgc	tgaggccctg	ctcggctcca					611
Lys	Leu	Cys	Thr	Gly	Pro	Thr	Pro	Pro	Cys							
	115					120										
tagccacccc	aggctgctgc	agtctcaggc	ccagagaagc	tcggaaccca	gattcctctc											671
ccagcagact	catcccgccc	cccccccaga	gatcatgagc	cctgggtctct	ggcctccagg											731
accacaccag	atccacggga	tcagctgaag	aagtcacggg	actcgtcagc	gctcacaaga											791
tccactaagt	cgctcttggc	atctcaatac	cctcttctga	ataagagaag	tctattttcc											851
cgaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aa													883

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Gly	Lys	Pro	Ala	Leu	Gln	Tyr	Asn	Asp	Tyr	Gly	Cys	Tyr	Cys	Gly	Val	
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Gly Gly Ser His Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala  
 30 35 40 45

His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys  
 50 55 60

Leu Glu Lys Tyr Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala  
 65 70 75

Gly Arg Thr Ala Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala  
 80 85 90

Ala Leu Cys Phe Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala  
 95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys  
 110 115 120

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tcctgggaga aggaggggaag cctgggggca cctggaaaat tcaggctgat ctctcctctg 180  
ggctactttg ggctcgnngg ccccgagcag cccctgggtcc agcccagcct ggctcacagg 240  
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atg aaa tct ccc cac gtg ctg gtg ttc ctt tgc ctc ctg gtg gct ctg 106  
Met Lys Ser Pro His Val Leu Val Phe Leu Cys Leu Leu Val Ala Leu  
-15 -10 -5

gtc acc ggg aac ctg gtt cag ttt ggg gtg atg atc gag aag atg aca 154  
Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr  
-1 1 5 10

ggc aag tcc gcc ctg cag tac aac gac tat ggc tgt tac tgc ggc atc 202

Gly	Lys	Ser	Ala	Leu	Gln	Tyr	Asn	Asp	Tyr	Gly	Cys	Tyr	Cys	Gly	Ile	
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Gly	Gly	Ser	His	Trp	Pro	Val	Asp	Gln	Thr	Asp	Trp	Cys	Cys	His	Ala	
30					35					40					45	
cac	gac	tgc	tgc	tac	ggg	cgt	ctg	gag	aag	ctg	ggc	tgt	gag	ccc	aaa	298
His	Asp	Cys	Cys	Tyr	Gly	Arg	Leu	Glu	Lys	Leu	Gly	Cys	Glu	Pro	Lys	
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ctg	gaa	aag	tat	ctt	ttc	tct	gtc	agc	gaa	cgt	ggc	att	ttc	tgc	gcc	346
Leu	Glu	Lys	Tyr	Leu	Phe	Ser	Val	Ser	Glu	Arg	Gly	Ile	Phe	Cys	Ala	
			65					70					75			
ggc	agg	acc	acc	tgc	cag	cgg	ctg	acc	tgc	gag	tgt	gac	aag	agg	gct	394
Gly	Arg	Thr	Thr	Cys	Gln	Arg	Leu	Thr	Cys	Glu	Cys	Asp	Lys	Arg	Ala	
		80					85					90				
gcc	ctc	tgc	ttt	cgc	cgc	aac	ctg	ggc	acc	tac	aac	cgc	aaa	tat	gcc	442
Ala	Leu	Cys	Phe	Arg	Arg	Asn	Leu	Gly	Thr	Tyr	Asn	Arg	Lys	Tyr	Ala	
	95					100					105					
cat	tat	ccc	aac	aag	ctg	tgc	acc	ggg	ccc	acc	ccg	ccc	tgc	tga		487
His	Tyr	Pro	Asn	Lys	Leu	Cys	Thr	Gly	Pro	Thr	Pro	Pro	Cys			
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Gly	Lys	Ser	Ala	Leu	Gln	Tyr	Asn	Asp	Tyr	Gly	Cys	Tyr	Cys	Gly	Ile	
15						20					25					



Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala  
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His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys  
 50 55 60

Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala  
 65 70 75

Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala  
 80 85 90

Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala  
 95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys  
 110 115 120

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